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Fuzzy Naive Bayesian model for Medical Diagnostic Decision Support

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***Abstract*— This work relates to the development of computational algorithms to provide decision support to physicians. The authors propose a Fuzzy Naive Bayesian (FNB) model for medical diagnosis, which extends the Fuzzy Bayesian approach proposed by Okuda. A physician's interview based method is described to define a orthogonal fuzzy symptom information system, required to apply the model. For the purpose of elaboration and elicitation of characteristics, the algorithm is applied to a simple simulated dataset, and compared with conventional Naive Bayes (NB) approach. As a preliminary evaluation of FNB in real world scenario, the comparison is repeated on a real fuzzy dataset of 81 patients diagnosed with infectious diseases.**

The case study on simulated dataset elucidates that FNB can be optimal over NB for diagnosing patients with imprecise-fuzzy information, on account of the following characteristics— 1) it can model the information that, values of some attributes are semantically closer than values of other attributes, and 2) it offers a mechanism to temper exaggerations in patient information. Although the algorithm requires precise training data, its utility for fuzzy training data is argued for. This is supported by the case study on infectious disease dataset, which indicates optimality of FNB over NB for the infectious disease domain. Further case studies on large datasets are required to establish utility of FNB.

I. INTRODUCTION

This work relates to the development of computational algorithms to provide decision support to physicians. Research on this problem was initiated five decades ago, with a probabilistic Bayesian model of physician's reasoning by Ledley and Lusted [1]. Ensuing pioneering work to develop and validate computer based decision support systems, used Naive Bayes (NB) [2], [3], followed by rule-based [4] and symbolic reasoning [5] approaches. In the last two decades, bayesian networks [6] and fuzzy set theory have been used to impart mathematical rigor to systems. For a historical review of Medical Decision Support research see Miller [7]. Later approaches include artificial neural networks [8], support vector machines [9], and information theory [10]. Overall Independence or Naive Bayes remains the most widely researched approach and many comparative studies have evaluated it as near optimal [11], [3], [12].

With the aim of improving the accuracy of diagnostic models, a soft computing approach using fuzzy relations [13], [14] was proposed by Sanchez [15]. Adlassnig [16] extended this approach and showed its utility with evaluative studies on Rheumatoid patients. Wagholikar and Deshpande in their recent case study [17] suggest a marginally improved accuracy of their alternative fuzzy relation based approach over Naive Bayes. Besides fuzzy relations, other fuzzy set theoretic concepts [18], [19] have been found useful for diagnosis.

In this manuscript we propose a Fuzzy Naive Bayesian (FNB) model for medical diagnosis, which extends the Fuzzy Bayesian approach proposed by Okuda [20]. A physician's interview based method is described to define an orthogonal fuzzy symptom information system, required to apply the model. For the purpose of elaboration and elicitation of characteristics, the algorithm is applied to a simple simulated dataset, and compared with conventional Naive Bayes (NB) approach. As a preliminary evaluation of FNB in real world scenario, the comparison is repeated on a real fuzzy dataset of 81 patients diagnosed with infectious diseases.

II. METHODS

A. Naive Bayes

From a training set of patient data, marginal probabilities of symptoms $P(s_i)$ and diseases $P(d_j)$, and conditional probabilities of symptoms on all diseases $P(s_i|d_j)$ are calculated by counting frequencies in the data. Given a set of symptoms ($S \equiv \{s_i\}$) for a patient, the posterior probability for each diagnosis for the patient is calculated as,

$$P(d_j|S) = P(d_j) \ \Pi_{s_i \in S} \ \frac{P(s_i|d_j)}{P(s_i)} \tag{1}$$

Since denominator $\Pi_{s_i \in S} \ P(s_i)$, is common in the computation of posterior probabilities for all diagnoses, it is dropped and a diagnostic score is computed for each diagnosis as,

$$P(d_j|S) = P(d_j) \ \Pi_{s_i \in S} \ P(s_i|d_j) \tag{2}$$

Conditional probability of symptom s_i for disease d_j is,

$$P(s_i|d_j) = \frac{f(s_i \cap d_j)}{f(d_j)} \tag{3}$$

where $f(d_j)$ is the number of patients in the dataset with disease d_j and $f(s_i \cap d_j)$ is the frequency count of patients with both s_i and d_j. Symptoms which are not reported in a particular disease, have zero condition probability for the disease. While calculating the diagnostic scores, the zero-probabilities wipe out the information from other symptoms, and hence to avoid this problem their zero conditional probabilities are corrected to 0.5 [21].

Differential diagnosis is output by ranking diagnoses in descending order of their corresponding computed diagnostic score and excluding the diagnoses below a cut-off rank.

B. Fuzzy Naive Bayes

When there is uncertainty about the description of a particular symptom for a given patient, the information is fuzzy and the particular piece of symptom information is referred to as fuzzy symptom description or simply fuzzy symptom. In contrast crisp symptoms are those which are certain. Each fuzzy symptom (indicated by underscore) is defined as a fuzzy set on the set of classical/crisp symptoms. The membership value of crisp symptom s_i in fuzzy symptom $\underline{s_k}$ is obtained by interviewing physicians with the question "What is your degree of belief in $\underline{s_k}$ when a patient asserts s_i"

For instance, fever can be described as absent (no), present (yes), or in terms of its grades–low and high. When symptom-descriptions are directly recorded from the patient, without an elaborate examination by the physician to establish the symptom, their values/grades are likely to be incorrect due to loose interpretations of the used vocabulary. The uncertainty resident in such information is vagueness or fuzziness [22], which is modeled by defining fuzzy sets for fuzzy descriptions of fever on the crisp descriptions of fever.

The fuzzy membership values are normalized as in equation 4, and the resulting fuzzy sets are said to form a orthogonal fuzzy symptom information system.

$$\mu_{\underline{s_i}} s_i = \frac{\mu_{\underline{s_k}} s_i}{\Sigma_i \mu_{\underline{s_k}} s_i} \tag{4}$$

In the orthogonal fuzzy information system the following relation is satisfied for all fuzzy-symptoms.

$$\Sigma_i \mu_{\underline{s_k}} s_i = 1 \tag{5}$$

The marginal probabilities of crisp-symptoms $P(s_i)$ and diseases $P(d_j)$, and conditional probabilities of crisp-symptoms on all diseases $P(s_i|d_j)$ are calculated as in the conventional NB method. The training data used for this purpose is required to have accurate symptom information. Conditional probabilities of fuzzy-symptoms $(\underline{s_k})$ for particular diagnosis (d_j), are calculated as,

$$P(\underline{s_k}|d_j) = \Sigma_i P(s_i|d_j) \mu_{\underline{s_k}} s_i \tag{6}$$

Marginal probability of fuzzy symptom $\underline{s_k}$ is,

$$P(\underline{s_k}) = \Sigma_i P(s_i) \mu_{\underline{s_k}} s_i \tag{7}$$

When the information given for a patient test case is fuzzy $\underline{S} \equiv \{\underline{s_k}\}$, the posterior probability for each diagnosis for the case is calculated using,

$$P(d_j|\underline{S}) = P(d_j)\, \Pi_{\underline{s_k} \in \underline{S}}\, \frac{P(\underline{s_k}|d_j)}{P(\underline{s_k})} \tag{8}$$

Since denominator $\Pi_{\underline{s_k} \in \underline{S}}\, P(\underline{s_k})$, is common for all diagnoses, it is dropped and a diagnostic score is computed for each diagnosis as,

$$P(d_j|\underline{S}) = P(d_j)\, \Pi_{\underline{s_k} \in \underline{S}}\, P(\underline{s_k}|d_j) \tag{9}$$

TABLE I

CONDITIONAL PROBABILITIES OF CRISP SYMPTOMS ON DIAGNOSES

	cough		fever	
	no	yes	low	high
Malaria	1	0.5	0.5	1
Tuberculosis	0.5	1	1	0.5

TABLE II

FUZZY SYMPTOM MEMBERSHIPS FROM PHYSICIAN'S INTERVIEW

	Crisp Symptoms			
Fuzzy Symptoms	no cough	cough	low fever	high fever
no cough	.9	.1	0	0
cough	.2	.9	0	0
low fever	0	0	.9	.4
high fever	0	0	.5	.9

As in the conventional NB, differential diagnosis is output by ranking diagnoses, in descending order of their computed diagnostic score and using a rank cut-off.

C. Case study on simulated dataset

To elucidate the differences in FNB and NB approaches, we describe their application to a simple simulated dataset, limited to two diagnoses– Malaria and Tuberculosis and two symptoms– fever and cough. Assume that a training set having equal number of Malaria and Tuberculosis cases is obtained by an elaborate examination to establish the symptoms. The Malaria patients have high-grade fever and no cough, which is typical for the disease [23], [24], and the Tuberculosis cases have the characteristic complaints of low-grade fever and cough [23], [24]. Since information in the training set has a high degree of precision, frequency counts on the training set will give accurate estimates for probabilities. The marginal probabilities of symptoms and diagnoses are 0.5 and conditional probabilities of symptoms are shown in table I. For applying FNB, fuzzy symptom sets were defined by interviewing a physician, as shown in table II. Applying equation 4, an orthogonal fuzzy symptom information system is obtained (table III). The conditional probabilities of fuzzy symptoms are calculated using 6 (table IV). Now we consider a test set comprised of cases which are not elaborately examined to establish their symptoms and the patient's narration is accepted verbatim. Such patient information is fuzzy, with some patients incorrectly grading their symptoms. Let the test set contain few such instances,

TABLE III

ORTHOGONAL FUZZY SYMPTOM INFORMATION SYSTEM

	Crisp Symptoms			
Fuzzy Symptoms	no cough	cough	low fever	high fever
no cough	.9	.1	0	0
cough	.18	.82	0	0
low fever	0	0	.69	.31
high fever	0	0	.36	.64

TABLE IV

CONDITIONAL PROBABILITIES OF FUZZY SYMPTOMS ON DIAGNOSES

	cough		fever	
	no	yes	low	high
Malaria	.95	.591	.654	.821
Tuberculosis	.550	.909	.846	.679

TABLE V

SYMPTOM DESCRIPTIONS OF TEST CASES

	cough	fever
Typical Malaria	no	high
Typical Tuberculosis	yes	low
Atypical Malaria	no	low

wherein the patient having malaria mistakenly reports no cough and low fever— interchanging low fever for high fever. This particular case is referred to as atypical case of Malaria. We apply NB and FNB to this atypical case and to the typical cases of Malaria and Tuberculosis described above (see table V), and compute the posterior probabilities for the diagnoses for each test case. For example while applying NB to typical Malaria case, $P(\text{Malaria}|\text{no cough} \cap \text{high fever})$
$= P(\text{Malaria})\text{x}P(\text{no cough}|\text{Malaria})\text{x}P(\text{high fever}|\text{Malaria})$
$= .5 \text{ x } 1 \text{ x } 1 = .5$

D. Case sudy on Real dataset

FNB method requires the assumption that the training dataset is precise. However in the real world precision in data is rarely practicable. Hence, to investigate the effect of relaxing this assumption, we evaluated FNB on a real fuzzy dataset. Comparison of FNB with NB was repeated for a real dataset of 81 patients diagnosed with 16 different infectious diseases. An elaborate examination to establish the symptoms in the patients was not carried out, and the entire dataset was fuzzy. For evaluation, a Jackknife was performed and Area under Receiver Operating Characteristic (ROC) curve for both methods [25] was calculated. To avoid querying for cases not adequately represented in the training set, cases for diseases having less than 5 instances in the dataset were excluded from testing. Hence, there were a total of 67 queries for 7 different diagnoses (see table VI). The computations were done using Ruby scripts, developed for the purpose.

III. RESULTS AND DISCUSSION

A. Case Study on Simulated Dataset

Results (see table VII) show that FNB correctly diagnoses the atypical case of Malaria, while NB is ambiguous as it computes equal scores for the diagnoses.

Table II, embodies the information that the modifiers low and high for fever are closer in meaning to each other as compared, to the modifiers no and yes for cough. This has an effect of decreasing the power of fever to discriminate between the diseases, as can been seen in table IV, where the difference in conditional probabilities of fuzzy symptoms-

TABLE VI

DISTRIBUTION OF QUERIES FROM INFECTIOUS DISEASES DATASET

Diagnosis	Count
AGE with dehydration	12
Amoebiasis	6
Chicken pox	7
Hepatitis B	5
Measles	19
Pulmonary Kochs	9
Typhoid	9

TABLE VII

DIAGNOSTIC SCORES FOR TYPICAL AND ATYPICAL CASES USING CONVENTIONAL NAIVE BAYES(NB) AND FUZZY NAIVE BAYES(FNB)

Test case	NB			FNB		
	M	T	Computed	M	T	Computed
Typical Malaria	.5	.12	M	.39	.19	M
Typical Tuberculosis	.12	.5	T	.19	.39	T
Atypical Malaria	.25	.25	-	.31	.23	M

M – Malaria, T – Tuberculosis

low fever and high fever is less than the difference for fuzzy symptoms- cough and no cough; while the differences are equal for their crisp counterparts (table I).

Moreover table II, captures the physician's belief that patients not having cough are more likely to report its presence, than the other way round. Hence, a complaint of cough should be more strongly interpreted as no cough than vice-versa. Similarly, patients having high grade fever are less likely to report it as low grade fever. It captures a widely held belief in the medical community, that patients often emphasize and exaggerate their problems [26], [27]. A consequence of modeling such information in FNB is that, the influence of higher gradations of symptoms, on the diagnostic computations is tempered, which filters out exaggerations in patient information. Table VIII demonstrates this effect of biasing the fuzzy symptom memberships towards lower symptom grades. μ is the membership value of crisp symptom-high fever in fuzzy symptom low fever. The diagnostic scores for Malaria and Tuberculosis are shown with the Odds score for Malaria, for the Typical case of Malaria complaining of high fever, and no cough. When $\mu = .5$ which equals the membership grade of crisp-symptom low fever in fuzzy-symptom high fever, the bias towards mild grades is removed, and consequently the odds for Malaria is found to reduce from 2.24 to 2.09. FNB uses precise

TABLE VIII

EFFECT OF BIASING THE FUZZY SYMPTOM MEMBERSHIPS TOWARDS LOWER SYMPTOM GRADES

μ	Malaria	Tuberculosis	Odds for Malaria
.5	.3902	.1866	2.09
.4	.4019	.1798	2.24

μ– membership of crisp symptom high-fever in fuzzy symptom low-fever

training data to compute posterior probabilities of diagnoses for fuzzy test cases. However, we argue that it may still be useful to train FNB on a imprecise-fuzzy dataset, since the noisy individual cases will cancel out each others mislabeled attributes, leading to reduced errors in frequency counts and consequentially to fairly accurate probability estimates.

B. Case Study on Real Dataset

The M-measures obtained for NB and FNB were .48 and .51 respectively, which indicates that FNB is marginally optimal over NB, for the described domain. M-measure is a cut-off independent [25] measure of accuracy and is especially suitable for comparing algorithms for differential medical diagnoses [25]. The results demonstrate utility of FNB for training on fuzzy data. However, the dataset is small and studies on large datasets are required for drawing definitive conclusions.

C. Limitations

The described interview based approach to obtain fuzzy symptom memberships is unfeasible for domains having large number of attributes. Hence, automated methods to compute the memberships from data are required.

IV. CONCLUDING REMARKS

The case study on simulated dataset elucidates that FNB can be optimal over NB for diagnosing patients with imprecise-fuzzy information, on account of the following characteristics—1) it can model the information that values of some attributes are semantically closer than values of other attributes, and 2) it offers a mechanism to temper exaggerations in patient information. Although the algorithm requires precise training data, its utility for fuzzy training data is argued for. This is supported by the case study on infectious disease dataset, which indicates optimality of FNB over NB for the infectious disease domain. Further studies on large datasets, are required to establish utility of FNB. The method may be particularly useful for inference from linguistic data, as such data is inherently fuzzy.

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